#12/13/02

FILE NO. A34701 (070050.1728)
PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Fisher *et al.*		
Serial No.	:	09/724,028	Examiner:	Tung, Joyce
Filed	:	November 28, 2000	Group Art Unit:	1637
For	:	METHOD FOR FULL-LENGTH cDNA CLONING USING DEGENERATE STEM LOOP ANNEALING PRIMERS		

RESPONSE TO RESTRICTION REQUIREMENT

I hereby certify that this paper is being deposited with the United States Postal Service as first class mail in an envelope addressed to:
Assistant Commissioner for Patents, Washington, D.C. 20231

December 2, 2002
Date of Deposit

Lisa B. Kole
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35,225
PTO Registration No.

Signature

December 2, 2002
Date of Signature

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

In response to the Restriction Requirement dated October 2, 2002, please consider the following remarks. Applicants submit herewith a Petition requesting a one-month extension of time for this response up to and including Monday, December 2, 2002, and accordingly authorize payment in the amount of $55.00 as required for a small entity under

37 C.F.R. §1.17(a)(1).

The Examiner asserts that that the present application contains three distinct inventions, grouped as follows:

Group I: Claims 1-7 and 16-17, drawn to a method for isolating a double stranded cDNA having a nucleotide sequence of a complete open reading frame from an isolated single stranded cDNA or mRNA, classified in class 435, sub-class 91.2/91.51.

Group II: Claims 8-14, drawn to a method of generating a cDNA library from a population of single stranded cDNA molecules, classified in class 435, subclass 91.2.

Group III: Claim 15, drawn to a kit for generating a complete open reading frame double stranded cDNA of interest containing nucleic acid primers, classified in class 435, subclass 810.

The Examiner indicates that these three Groups do not relate to a single invention under 35 U.S.C. § 121 because each of the Groups may be used separately from each other. For example, according to the Examiner, the invention of Group I is a method of isolating a double stranded cDNA molecule having a complete open reading frame from isolated single stranded cDNA or mRNA molecules, while the invention of Group II is a method for generating a cDNA library. The invention of Group III, according to the Examiner, is distinct from the inventions of Groups I and II because it is a kit that can be used for nucleic acid

purification. The Examiner has therefore required that Applicants restrict the prosecution of this application to one of the foregoing groups.

In response, Applicants elect to pursue in this application the invention of Group I, which comprises Claims 1-7 and 16-17 as they relate to a method for isolating a double stranded cDNA having a nucleotide sequence of a complete open reading frame from an isolated single stranded cDNA or mRNA molecule. This election is made without traverse, and without prejudice to the prosecution of the subject matter of the non-elected groups in other patent applications.

The Examiner has further indicated that the instant application contains claims directed to a plurality of disclosed patentably-distinct restriction groups comprising different, but unspecified, SEQ ID NOs, and maintains that Applicants are required under 35 U.S.C. § 121 to elect no more than one of the disclosed nucleic acids representing one different SEQ ID NO even though this requirement may be traversed.

In response, Applicants respectfully note that the Examiner has indicated that Claims 1-7 and 16-17 constitute a single invention (Group I), namely a method for isolating a double stranded cDNA having a nucleotide sequence of a complete open reading frame from an isolated single stranded cDNA or mRNA. The specification discloses that this method may be practiced using one of several primers tailored to different conditions. These primers are depicted as D-SLAP, D-CLAP1, D-CLAP2, and T-SLAP in Figure 1A.

D-SLAP and T-SLAP are related, in that the random sequence of twelve nucleotides at the 3' end of the D-SLAP primer is twelve thymidine nucleotides for the T-SLAP primer. Thus, T-SLAP is merely a variant of D-SLAP.

Similarly, D-CLAP1 and D-CLAP2 are also related, in that the random sequence of twelve nucleotides at the 3' end of the D-CLAP2 primer is three guanidine nucleotides followed by nine random nucleotides in D-CLAP1. D-CLAP1 is therefore but one of the many possible variants of D-CLAP2.

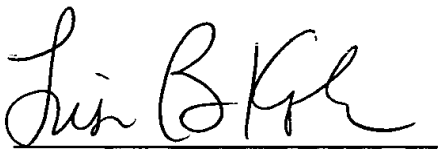
The use of the D-SLAP, D-CLAP1 and D-CLAP2 primers in the method of Claim 1 is claimed in dependent Claims 3, 4 and 5, respectively, of Group I. Applicants are therefore unsure as to how they may comply with the Examiner's two requests to elect a single inventive group and a single nucleic acid species. For example, if Applicants elect, in the present application, Group I, which comprises Claims 1-7, 16 and 17, and then further limit this group election to the nucleic acid sequence of D-SLAP, it seems that they will be denied, at least in the present application, the ability to pursue Claims 4 and 5, which the Examiner has otherwise indicated are a permissible subject of this invention. In the alternative, if the Examiner intended the Applicants' invention to be limited in a single application to the use of one of the primers selected from the group consisting of D-SLAP, D-CLAP1, D-CLAP2 or T-CLAP for the isolation from single stranded cDNA or mRNA of double stranded cDNAs having a complete open reading frame, then Applicants are unclear

as to why Claims 3, 4 and 5 could constitute part of a single inventive entity. Clarification of this issue is respectfully requested.

Because Applicants have been advised that, in order to be deemed responsive, a reply to this requirement must include an identification of the species that is elected, Applicants elect with traverse the sequence of the D-SLAP primer as disclosed in Claim 3 of Group I (SEQ ID NO:1).

Respectfully submitted,

BAKER BOTTS L.L.P.



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